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Correlation and Path Analysis for Yield Attributing Characters in Early Maturing Genotypes of Rice (*Oryza sativa* L.)

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Abstract

Association analysis was studied for yield attributing traits in the early maturing rice accessions. The study showed that grain yield per plot had positive significant correlation with culm length (cm), number of secondary branches per panicle, flag leaf length (cm) and spikelet fertility percentage. It showed that one should direct select these traits for crop improvement. Path analysis that the traits Culm length (cm), Spikelet fertility percentage, Flag leaf length (cm), Number of secondary branching per panicle, days to 50% flowering to maturity had positive direct effect coupled with positive significant correlation with grain yield per plant. Therefore, simultaneous improvement of grain yield is possible through selection of this trait. The trait average internodal length also recorded direct positive effects but have positive non-significant correlation. Hence indirect factors are to be considered for improving the yield.

Key words : *Correlation, path analysis, yield attributes, genotypes, rice.*

Introduction

Rice (*Oryza sativa* L.) is a major food crop worldwide. More than half of the world's population eats it as a staple diet. Rice is the world's second-most-produced cereal crop. Rice is cultivated worldwide over an area of about 162.06 m ha with an annual production of about 505 milliontonnes and average productivity of 26.59q. (1). India has acreage of 43.82 m ha with total production 112.44 m t and an average productivity of 25.66 q (1). Chhattisgarh is popularly known as 'Rice bowl of India', this state occupies an area of 3.90 m ha and productivity of 34.38 q (2).

The measure of the mutual relationship between two variables is called as correlation. It is a metric for determining the degree of similarity and linear connection between two variables. The study of correlations may help the plant breeder to improve one character and associated characters. The correlation coefficient will not be as true and justified, until we got the similar results from Path coefficient analysis. Path coefficient analysis is the correlation values through direct and indirect dependent variables.

Materials and Methods

The experimental material comprises of thirty-nine rice genotypes of early maturity duration groupswith four checks: Local check (Chandrahasini), National check (Gontrabidhan-3), Zonal check (MTU-1010) and Hybrid check (US-312). The genotypes were raised in RBD with 3 replications at BTC College of Agriculture and Research Station, Bilaspur, Chhattisgarh. Each replication was grown with the plot size 1.0 m × 10.0 m (10 m^2) and the row to row spacing was maintained to be 20 cm for each plot in each replication. Observations were recorded on days to 50% flowering to maturity, culm length(cm), number of tillers per meter square, main panicle length (cm), awn length (cm), flag leaf length (cm), average internodal length (cm), test weight (g), spikelet fertility percentage (%), panicle shattering percentage (%), grain yield (kg/plot).

Study of character association helps the breeder in selection for grain yield in parent lines. It was estimated by formula given by (3).

Path coefficient analysis was suggested by Wright (1918) and expanded by (4). In which direct and indirect effects of independent variables were estimated.

Results and Discussion

The study on association analysis of the characters exhibited that the traits culm length (cm), number of secondary branches per panicle, flag leaf length (cm) and spikelet fertility percentage showed significant positive association with grain yield at both genotypic and phenotypic levels which showed that one should direct select these traits for crop improvement and can be practised. Negative and significant correlation of grain yield was found with the characters days to 50% flowering and days to maturity indicating that they have less influence on yield. Grain yield was observed positive

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Table-1 : Phenotypic correlation matrix.

Traits	DF	DM	DFM	CM	TMS	MPL	SBP	AL	FLL	AIL	TW	SFP	PSP	GYP
DF	1.000	0.909**	-0.460**	0.149	-0.195*	-0.190*	-0.252**	0.173	-0.139	-0.195*	-0.194*	-0.572**	0.208*	-0.261**
DM		1.000	-0.049	0.152	-0.208*	-0.148	-0.326**	0.277**	-0.140	-0.229*	-0.115	-0.550**	0.115	-0.260**
DFM			1.000	-0.032	0.026	0.138	-0.089	0.175	0.036	-0.021	0.220*	0.200*	-0.255**	0.070
CM				1.000	0.013	0.011	0.087	0.140	-0.067	-0.127	0.077	0.160	0.010	0.313**
TMS					1.000	0.133	0.052	0.113	-0.106	0.173	0.090	0.217*	-0.095	0.275**
MPL						1.000	-0.035	0.302**	-0.011	0.108	0.027	0.150	0.027	0.038
SBP							1.000	-0.190*	0.039	0.032	-0.232*	0.259**	0.212*	0.553**
AL								1.000	0.015	-0.271**	0.341**	0.146	-0.224*	-0.026
FLL									1.000	-0.042	0.046	0.028	-0.120	0.206*
AIL										1.000	-0.126	0.116	-0.009	0.033
TW											1.000	0.267**	-0.438**	0.058
SFP												1.000	-0.073	0.507**
PSP													1.000	-0.096

* Significant at 5% probability level, ** Significant at 1% probability level,
R critical value at 5% level of significance- ± 0.1816, R critical value at 1% level of significance- ±0.2373
DF = days to flowering, DM = days to maturity, DFM = days to flowering to maturity, CM = culm length (cm), TMS = number of tillers per meter square, MPL = main panicle length(cm), AL = awn length(cm), FLL = flag leaflength(cm), AIL = average internodal length(cm), TW = test weight (g), SFP = spikelet fertility percentage, PSP = panicle shattering percentage, GYP = grain yield per plot (kg)

Table-2 : Genotypic correlation matrix.

Traits	DF	DM	DFM	CM	TMS	MPL	SBP	AL	FLL	AIL	TW	SFP	PSP	GYP
DF	1.000	0.974**	-0.429**	0.160	-0.338**	-0.279**	-0.337**	0.201*	-0.145	-0.288**	-0.232*	-0.647**	0.215*	-0.354**
DM		1.000	-0.212*	0.159	-0.319**	-0.207*	-0.389**	0.291**	-0.161	-0.337**	-0.136	-0.597**	0.118	-0.334**
DFM			1.000	-0.054	0.187*	0.377**	-0.099	0.295**	-0.015	-0.098	0.455**	0.405**	-0.457**	0.197*
CM				1.000	-0.003	-0.004	0.083	0.143	-0.071	-0.230*	0.077	0.160	0.012	0.354**
TMS					1.000	0.201*	-0.052	0.198*	-0.084	0.386**	0.121	0.244**	-0.174	-0.015
MPL						1.000	-0.038	0.445**	0.172	0.322**	0.042	0.192*	0.043	0.064
SBP							1.000	-0.210*	0.091	0.122	-0.271**	0.262**	0.226*	0.631**
AL								1.000	0.026	-0.439**	0.355**	0.143	-0.230*	-0.016
FLL									1.000	-0.193*	0.086	0.074	-0.132	0.370**
AIL										1.000	-0.270**	0.204*	-0.062	0.047
TW											1.000	0.288**	-0.467**	0.039
SFP												1.000	-0.082	0.580**
PSP													1.000	-0.115

* Significant at 5% probability level, ** Significant at 1% probability level,
R critical value at 5% level of significance- ± 0.1816, R critical value at 1% level of significance- ±0.2373

Table-3 : Genotypic Path Matrix.

Traits	DF	DM	DFM	CM	TMS	MPL	SBP	AL	FLL	AIL	TW	SFP	PSP	GYP
DF	-0.108	0.317	-0.057	0.044	0.023	0.021	-0.186	-0.009	-0.053	-0.036	0.009	-0.289	-0.031	-0.354**
DM	-0.105	0.326	-0.028	0.044	0.021	0.015	-0.215	-0.013	-0.058	-0.042	0.005	-0.267	-0.017	-0.334**
DFM	0.046	-0.069	0.132	-0.015	-0.013	-0.028	-0.055	-0.013	-0.006	-0.012	-0.018	0.181	0.065	0.197*
CM	-0.017	0.052	-0.007	0.274	0.000	0.000	0.046	-0.006	-0.026	-0.029	-0.003	0.072	-0.002	0.354**
TMS	0.036	-0.104	0.025	-0.001	-0.067	-0.015	-0.029	-0.009	-0.030	0.048	-0.005	0.109	0.025	-0.015
MPL	0.030	-0.068	0.050	-0.001	-0.013	-0.074	-0.021	-0.019	0.062	0.040	-0.002	0.086	-0.006	0.064
SBP	0.036	-0.127	-0.013	0.023	0.003	0.003	0.553	0.009	0.033	0.015	0.011	0.117	-0.032	0.631**
AL	-0.022	0.095	0.039	0.039	-0.013	-0.033	-0.116	-0.043	0.009	-0.055	-0.014	0.064	0.033	-0.016
FLL	0.016	-0.053	-0.002	-0.020	0.006	-0.013	0.050	-0.001	0.362	-0.024	-0.003	0.033	0.019	0.370**
AIL	0.031	-0.110	-0.013	-0.063	-0.026	-0.024	0.068	0.019	-0.070	0.124	0.011	0.091	0.009	0.047
TW	0.025	-0.044	0.060	0.021	-0.008	-0.003	-0.150	-0.015	0.031	-0.034	-0.040	0.129	0.066	0.039
SFP	0.070	-0.195	0.053	0.044	-0.016	-0.014	0.145	-0.006	0.027	0.025	-0.011	0.448	0.012	0.580**
PSP	-0.023	0.038	-0.060	0.003	0.012	-0.003	0.125	0.010	-0.048	-0.008	0.019	-0.037	-0.142	-0.115

R Square = 0.8126, Residual Effect = 0.4329

DF = days to flowering, DM = days to maturity, DFM = days to flowering to maturity, CM = culm length (cm), TMS = number of tillers per meter square, MPL = main panicle length (cm), AL= awn length (cm), FLL = flag leaflength (cm), AIL = average internodal length (cm), TW = test weight (g), SFP = spikelet fertility percentage, PSP = panicle shattering percentage, GYP = grain yield per plot (kg).

Table-4 : Phenotypic Path Matrix.

Traits	DF	DM	DFM	CM	TMS	MPL	SBP	AL	FLL	AIL	TW	SFP	PSP	GYP
DF	-80.507	65.323	15.449	0.028	-0.046	-0.014	-0.127	-0.038	-0.032	0.008	-0.004	-0.260	-0.041	-0.261**
DM	-73.195	71.850	1.638	0.029	-0.049	-0.011	-0.163	-0.061	-0.032	0.010	-0.003	-0.250	-0.022	-0.260**
DFM	37.057	-3.506	-33.563	-0.006	0.006	0.010	-0.045	-0.039	0.008	0.001	0.005	0.091	0.050	0.070
CM	-11.972	10.926	1.090	0.189	0.003	0.001	0.044	-0.031	-0.015	0.005	0.002	0.073	-0.002	0.313**
TMS	15.738	-14.923	-0.875	0.003	0.235	0.010	0.026	-0.025	-0.024	-0.007	0.002	0.099	0.019	0.275**
MPL	15.256	-10.664	-4.635	0.002	0.031	0.075	-0.017	-0.067	-0.003	-0.005	0.001	0.068	-0.005	0.038
SBP	20.309	-23.391	2.986	0.017	0.012	-0.003	0.501	0.042	0.009	-0.001	-0.005	0.118	-0.042	0.553**
AL	-13.912	19.867	-5.874	0.026	0.027	0.023	-0.095	-0.221	0.004	0.012	0.008	0.066	0.044	-0.026
FLL	11.200	-10.045	-1.196	-0.013	-0.025	-0.001	0.020	-0.003	0.230	0.002	0.001	0.013	0.024	0.206*
AIL	15.682	-16.445	0.697	-0.024	0.041	0.008	0.016	0.060	-0.010	-0.043	-0.003	0.053	0.002	0.033
TW	15.647	-8.295	-7.385	0.015	0.021	0.002	-0.117	-0.075	0.011	0.005	0.023	0.121	0.086	0.058
SFP	46.048	-39.482	-6.727	0.030	0.051	0.011	0.130	-0.032	0.007	-0.005	0.006	0.455	0.014	0.507**
PSP	-16.748	8.232	8.549	0.002	-0.022	0.002	0.106	0.050	-0.028	0.000	-0.010	-0.033	-0.196	-0.096

R Square = 0.6299 Residual Effect = 0.6084, Bold values shows direct effect normal values shows indirect effect

*Significant at 5% probability level, ** Significant at 1% probability level,

R critical value at 5% level of significance- ± 0.1816, R critical value at 1% level of significance- ±0.2373 significant with the reference of (5) for days to 50% flowering. (6) for days to maturity. (7) for flag leaf length. (8) for grain yield (kg/plot). The correlation coefficient was represented in Table-1 and 2.

Path coefficient analysis indicated that highest positive direct effect on grain yield per plant at genotypic levels was exhibited by the character number of secondary branches per panicle (0.553), spikelet fertility percentage (0.448), flag leaf length (cm) (0.362), culm length (cm) (0.274) and the rest of the characters showed low magnitude of direct effects. At phenotypic levels, number of secondary branches per panicle (0.501), spikelet fertility percentage (0.455), number of tillers per square meter (0.235), flag leaf length (cm) (0.230), culm length (cm) (0.189), main panicle length (cm) (0.075), test weight (g) (0.023). Similar findings were found by (9,10) for days to maturity, (11) for culm length (cm), (10) for number of secondary branches per panicle, (12) for flag leaf length, (13) for spikelet fertility percentage. It shows that these characters were directly influence the grain yield, while other characters were indirectly influencing grain yield.

The direct and indirect effects of different characters are represented in Table-3 and 4. Test weight showed positive direct effect at phenotypic level (14). Panicle shattering percentage had negative direct effect on grain yield per plot with non-significant negative association revealed that shattering of panicles reduces grain yield.

The path analysis showed that no common factor was there which directly influence the grain yield per plot but sum factors such as days to maturity, culm length (cm), number of secondary branches per panicle, flag leaf length (cm) and spikelet fertility percentage could be effective for increment in grain yield and could be used for selection.

Residual Effects : The residual effect determines how well the causal factors explain for the variability of the next dependent factor, which in this case is grain yield per plot. In present study residual effect was 0.433 and 0.608 at genotypic and phenotypic level respectively. The residual effect 0.433 at genotypic and 0.608 at phenotypic level indicates that the nine traits explain 57 per cent and 39 per cent of variability in grain yield per plant.

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